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## RAW SEQUENCE LISTING

DATE: 05/16/2002

PATENT APPLICATION: US/09/658,835A

TIME: 16:57:01

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\05162002\I658835A.raw

```

3 <110> APPLICANT: Duvick, Johnathan P.
4   Gilliam, Jacob T.
5   Maddox, Joyce R.
6   Rao, Aragula Gururaj
7   Crasta, Oswald R.
8   Folkerts, Otto
10 <120> TITLE OF INVENTION: Amino Polyol Aamine Oxidase Polynucleotides and Related
Polypeptides and
11   Methods of Use
13 <130> FILE REFERENCE: 1134R
15 <140> CURRENT APPLICATION NUMBER: US 09/658,835A
C--> 16 <141> CURRENT FILING DATE: 2002-05-03
18 <150> PRIOR APPLICATION NUMBER: US 60/092,936
19 <151> PRIOR FILING DATE: 1998-07-25
21 <150> PRIOR APPLICATION NUMBER: US 60/135,391
22 <151> PRIOR FILING DATE: 1999-05-21
24 <150> PRIOR APPLICATION NUMBER: US 09/352,159
25 <151> PRIOR FILING DATE: 1999-07-12
27 <150> PRIOR APPLICATION NUMBER: US 09/352,168
28 <151> PRIOR FILING DATE: 1999-07-12
30 <160> NUMBER OF SEQ ID NOS: 53
32 <170> SOFTWARE: PatentIn version 3.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 372
36 <212> TYPE: DNA
37 <213> ORGANISM: Exophiala spinifera
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40 <221> NAME/KEY: misc_feature
41 <222> LOCATION: (346)..(346)
42 <223> OTHER INFORMATION: n = A, T, C, or G
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48 gcttggactg ttgggaccac ttccgtcccg ggtctccgac catgaaacag gtaatggacc      120
50 attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatgggggtca cagctcgatt      180
52 ggaaggacgc cgagaagcct tgttcgcgcc accacggctt gtcccatagc aagactatct      240
54 tgctatagta gccacggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg      300
W--> 56 gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc tttttgcttc      360
58 ggaacacggc gc
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63 <212> TYPE: DNA
64 <213> ORGANISM: Exophiala spinifera
66 <400> SEQUENCE: 2
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69 tacaagggttg tggtaacga aaccaccacc tttttgcttc ggaacacggc gcccaggcc 120
71 gatcgtactg tacagccgga tgcgactgc tcaatttcag cgacgggggt gttgaggtgc 180
73 ac 182
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77 <211> LENGTH: 29
78 <212> TYPE: DNA
C--> 79 <213> ORGANISM: Artificial
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Designed oligonucleotide for 3' RACE N21965
84 <400> SEQUENCE: 3
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88 <210> SEQ ID NO: 4
89 <211> LENGTH: 28
90 <212> TYPE: DNA
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93 <220> FEATURE:
94 <223> OTHER INFORMATION: Designed oligonucleotide for 5' RACE 21968
96 <400> SEQUENCE: 4
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102 <212> TYPE: DNA
103 <213> ORGANISM: Exophiala spinifera
105 <220> FEATURE:
106 <221> NAME/KEY: CDS
107 <222> LOCATION: (1)..(1386)
108 <223> OTHER INFORMATION:
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112 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
113 1 5 10 15
115 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
116 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
117 20 25 30
119 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
120 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
121 35 40 45
123 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
124 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
125 50 55 60
127 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
128 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
129 65 70 75 80
131 ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288
132 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
133 85 90 95
135 ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336
136 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
137 100 105 110

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139	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	384
140	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	
141			115					120					125				
143	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	432
144	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	
145		130					135					140					
147	ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	480
148	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	
149	145					150					155				160		
151	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt	528
152	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	
153					165					170				175			
155	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	576
156	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	
157			180					185					190				
159	agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	624
160	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	
161			195				200					205					
163	cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	atg	672
164	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	
165		210				215				220							
167	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	720
168	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	
169	225					230				235				240			
171	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	768
172	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	
173					245					250				255			
175	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	ggt	tcg	tta	ccg	aca	acc	ttg	816
176	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	
177			260					265					270				
179	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	864
180	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	
181			275				280					285					
183	ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	912
184	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	
185		290				295				300							
187	tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	960
188	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	
189	305					310				315				320			
191	tcg	agc	tgt	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	1008
192	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	
193					325					330				335			
195	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	1056
196	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	
197			340					345					350				
199	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac	1104
200	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	
201			355				360					365					
203	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	1152

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204 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
205      370      375      380
207 gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga      1200
208 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
209 385      390      395      400
211 gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg      1248
212 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
213      405      410      415
215 gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg      1296
216 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
217      420      425      430
219 tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa      1344
220 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
221      435      440      445
223 cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag      1389
224 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
225      450      455      460
228 <210> SEQ ID NO: 6
229 <211> LENGTH: 462
230 <212> TYPE: PRT
231 <213> ORGANISM: Exophiala spinifera
233 <400> SEQUENCE: 6
235 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
236 1      5      10      15
239 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
240      20      25      30
243 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
244      35      40      45
247 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
248      50      55      60
251 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
252 65      70      75      80
255 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
256      85      90      95
259 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
260      100      105      110
263 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
264      115      120      125
267 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
268      130      135      140
271 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
272 145      150      155      160
275 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
276      165      170      175
279 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
280      180      185      190
283 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
284      195      200      205
287 Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met

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288      210      215      220
291 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
292 225      230      235      240
295 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
296      245      250      255
299 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
300      260      265      270
303 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
304      275      280      285
307 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
308      290      295      300
311 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
312 305      310      315      320
315 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
316      325      330      335
319 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
320      340      345      350
323 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
324      355      360      365
327 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
328      370      375      380
331 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
332 385      390      395      400
335 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
336      405      410      415
339 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
340      420      425      430
343 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
344      435      440      445
347 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
348      450      455      460
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352 <211> LENGTH: 1442
353 <212> TYPE: DNA
354 <213> ORGANISM: Exophiala spinifera
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357 <221> NAME/KEY: CDS
358 <222> LOCATION: (1)..(645)
359 <223> OTHER INFORMATION:
361 <220> FEATURE:
362 <221> NAME/KEY: Intron
363 <222> LOCATION: (646)..(698)
364 <223> OTHER INFORMATION:
366 <220> FEATURE:
367 <221> NAME/KEY: CDS
368 <222> LOCATION: (699)..(1439)
369 <223> OTHER INFORMATION:
371 <400> SEQUENCE: 7
372 gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg

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48

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/658,835A

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Input Set : A:\PTO.VSK.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 346  
Seq#:39; N Pos. 649  
Seq#:40; Xaa Pos. 216

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 10

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,12,13,14,15,34

## VERIFICATION SUMMARY

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:300  
L:79 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:91 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:1004 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
L:1017 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13  
L:1030 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
L:1042 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15  
L:5233 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34  
L:5768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:600  
L:5880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:208